



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: HUMAN MPL LIGAND

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-Apr-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: P0871P3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
55 60 65
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
70 75 80
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100 105 110
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115 120 125
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
145 150 155
Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160 165 170
Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
175 180 185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
190 195 200

Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
220 225 230

Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
235 240 245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
265 270 275

Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295 300 305

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310 315 320

Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TC TTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
CTGGAGCCCT TCTCCACCGG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG CTC CTC 239
Met Glu Leu Thr Glu Leu Leu Leu
-21 -20 -15

GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 278
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
-10 -5

5 AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 317
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
1 5 10

10 AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 356
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25

15 AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 395
Ser Gln Cys Pro Glu Val His Pro Arg Pro Thr Pro Val
30 35

20 CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 434
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
40 45 50

ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 473
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
55 60 65

25 GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 512
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
70 75

30 GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 551
Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
80 85 90

35 CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 590
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
95 100

CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 629
Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
105 110 115

40 ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 668
Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
120 125 130

45 TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 707
Phe Gln His Leu Arg Gly Lys Val Arg Phe Leu Met
135 140

50 CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 746
Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
145 150 155

CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 785
Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
160 165

5 ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824
Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
170 175 180

10 GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

15 GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
200 205

20 CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
210 215 220

ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980
Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
225 230

25 GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235 240 245

C' cont.

30 CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
250 255 260

35 GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097
Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
265 270

40 TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
275 280 285

CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175
Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
290 295

45 CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
300 305 310

50 CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
315 320 325

CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
 Gln Asn Leu Ser Gln Glu Gly
 330 332

5 TGCCGACATC AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC 1340
 CCTGGGAGAC AACTGGACAA GATTTCTTAC TTTCTCTGA AACCCAAAGC 1390
 10 CCTGGTAAAA GGGATACACA GGAAGTAAAA GGAATCATT TTCTACTGTA 1440
 CATATAAAC CTTCAAGAAGC TATTTTITTA AGCTATCAGC AATACTCATC 1490
 AGAGCAGCTA GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG 1540
 15 ATTCTCTACA TGCTCTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG 1590
 CCTGGCAGTT GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA 1640
 AAGGGTAATT TCCTTTGCTT CAAATCAAG GCCTTCCAAC GCCCCATCC 1690
 20 CCTTTACTAT CATCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC 1740
 TTTACTCTTG AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA 1790
 25 AAAAA 1795

cont.
 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
 -16 -15 -10 -5
 40 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
 1 5 10
 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
 15 20 25 26

45 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: Nucleic Acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91
Leu Leu Leu Val Val Met Leu
-16 -15 -10
CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
-5 1
CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
5 10 15
GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26
CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260
GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310
TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360
ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150
TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300

AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350

ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
50 55 60

Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
110 115 120

His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
125 130 135

Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
140 145 150

Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
155 160 165

Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly
170 175 180

Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly
 200 205 210
 5 Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr
 215 220 225
 Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
 230 235 240
 10 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser
 245 250 255
 Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly
 260 265 270
 15 Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu
 275 280 285
 Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
 290 295 300
 Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
 305 310 315
 25 Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
 320 325 330
 Glu Gly
 332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
 1 5 10 15
 Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
 20 25 30
 45 Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
 35 40 45
 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
 50 55 60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTGAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGA ATG GAG 143
Met Glu
-21 -20

CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT GCA GTG 182
Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-15 -10

GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT 221
Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys
-5 1 5

GAC CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC 260
 Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His
 10 15 20

5 CTC CTT CAC AGC CGA CTG AGT CAG TGT CCC GAC GTC GAC 299
 Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp
 25 30

10 CCT TTG TCT ATC CCT GTT CTG CTG CCT GCT GTG GAC TTT 338
 Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp Phe
 35 40 45

15 AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA CAG AGC AAG 377
 Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys
 50 55

20 GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG 416
 Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu
 60 65 70

GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC 455
 Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys
 75 80 85

25 CTC TCA TCC CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC 494
 Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg
 90 95

C' cont.

30 CTC CTC TTG GGG GCC CTG CAG GGC CTC CTA GGA ACC CAG 533
 Leu Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln
 100 105 110

35 GGC AGG ACC ACA GCT CAC AAG GAC CCC AAT GCC CTC TTC 572
 Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe
 115 120

40 TTG AGC TTG CAA CAA CTG CTT CGG GGA AAG GTG CGC TTC 611
 Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe
 125 130 135

CTG CTT CTG GTA GAA GGT CCC ACC CTC TGT GTC AGA CGG 650
 Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg
 140 145 150

45 ACC CTG CCA ACC ACA GCT GTC CCA AGC AGT ACT TCT CAA 689
 Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln
 155 160

50 CTC CTC ACA CTA AAC AAG TTC CCA AAC AGG ACT TCT GGA 728
 Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
 165 170 175

TTG TTG GAG ACG AAC TTC AGT GTC ACA GCC AGA ACT GCT 767
 Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
 180 185

5 GGC CCT GGA CTT CTG AGC AGG CTT CAG GGA TTC AGA GTC 806
 Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val
 190 195 200

10 AAG ATT ACT CCT GGT CAG CTA AAT CAA ACC TCC AGG TCC 845
 Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser
 205 210 215

15 CCA GTC CAA ATC TCT GGA TAC CTG AAC AGG ACA CAC GGA 884
 Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly
 220 225

20 CCT GTG AAT GGA ACT CAT GGG CTC TTT GCT GGA ACC TCA 923
 Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser
 230 235 240

CTT CAG ACC CTG GAA GCC TCA GAC ATC TCG CCC GGA GCT 962
 Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala
 245 250

25 TTC AAC AAA GGC TCC CTG GCA TTC AAC CTC CAG GGT GGA 1001
 Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly
 255 260 265

30 CTT CCT CCT TCT CCA AGC CTT GCT CCT GAT GGA CAC ACA 1040
 Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr
 270 275 280

35 CCC TTC CCT CCT TCA CCT GCC TTG CCC ACC ACC CAT GGA 1079
 Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly
 285 290

40 TCT CCA CCC CAG CTC CAC CCC CTG TTT CCT GAC CCT TCC 1118
 Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser
 295 300 305

ACC ACC ATG CCT AAC TCT ACC GCC CCT CAT CCA GTC ACA 1157
 Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr
 310 315

45 ATG TAC CCT CAT CCC AGG AAT TTG TCT CAG GAA ACA TAGCGC 1199
 Met Tyr Pro His Pro Arg Asn Leu Ser Gln Gly Thr
 320 325 330 331

G GGCCTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC 1240

AAGCTTCCCC AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT 1290

GCTTTCACCT AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT 1340
 AAAATTTTAG GAGCTATTTT TTTTAACT ATCAGCAATA TTCATCAGAG 1390
 CAGCTAGCGA TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT 1440
 TCT 1443

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
 -21 -20 -15 -10
 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
 -5 1 5
 Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
 10 15 20
 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
 25 30 35
 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
 40 45 50
 Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
 55 60 65
 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
 70 75 80
 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
 85 90 95
 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Gly Arg Thr
 100 105 110
 Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln
 115 120 125
 Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro
 130 135 140
 Thr Leu Cys Val Arg Thr Leu Pro Thr Thr Ala Val Pro Ser
 145 150 155

Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr
160 165 170

Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
175 180 185

Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile
190 195 200

Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile
205 210 215

Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His
220 225 230

Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp
235 240 245

Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu
250 255 260

Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His
265 270 275

Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser
280 285 290

Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met
295 300 305

Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
310 315 320

Arg Asn Leu Ser Gln Glu Thr
325 330 331

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
5 50 55 60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
65 70 75

Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
10 80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
15 95 100 105

Gly Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
110 115 120

Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val
20 125 130 135

Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg
140 145 150

Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln Leu Leu
25 155 160 165

Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
170 175 180

Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser
30 185 190 195

Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn
35 200 205 210

Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg
215 220 225

Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr
40 230 235 240

Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe
245 250 255

Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro
45 260 265 270

Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser
50 275 280 285

Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro
290 295 300

5 Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro
305 310 315

His Pro Val Thr Met Tyr Pro His Pro Arg Asn Leu Ser Gln Glu
320 325 330

10 Thr
331

(2) INFORMATION FOR SEQ ID NO:11:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

25 Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu
20 25 26

(2) INFORMATION FOR SEQ ID NO:12:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

40 Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:13:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGTCTGCCG TGAAGGACAT GG 22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His
20 23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15

Val Leu Leu Pro Ala Val Asp Phe
20 23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15
Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15
Cys Leu Ser Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
1 5 10 15
Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15

Asp Pro Asn Ala Ile Phe
20 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15

Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25